STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/538,038_
Source: _PY/10_
Date Processed by STIC: _6/16/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05
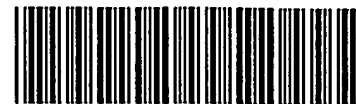
ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/538,038_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
    prevent "wrapping."

·2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
    Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
    ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
    each n or Xaa can only represent a single residue. Please present the maximum number of each
    residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
    the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
    Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped

    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
    (NEW RULES)   <210> sequence id number
    <400> sequence id number
    000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
    is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
    "Unknown." Please explain source of genetic material in <220> to <223> section.
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/538,038

DATE: 06/16/2005
TIME: 10:24:46

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\06162005\J538038.raw

[handwritten: IMPORTANT: see item 4 on Error Summary Sheet]

```
    3 <110> APPLICANT: Givaudan SA
    5 <120> TITLE OF INVENTION: G-Proteins
    7 <130> FILE REFERENCE: 30069P1
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/538,038
C-->  9 <141> CURRENT FILING DATE: 2005-06-08
    9 <160> NUMBER OF SEQ ID NOS: 2
   11 <170> SOFTWARE: PatentIn version 3.1
```

[handwritten: pp 1-2]

[handwritten stamp: Does Not Comply — Corrected Diskette Needed]

ERRORED SEQUENCES

[handwritten: delete numbers under codons. Use numbers under every 5.]

```
   13 <210> SEQ ID NO: 1
   14 <211> LENGTH: 1122
   15 <212> TYPE: DNA
   16 <213> ORGANISM: Homo sapiens
   18 <220> FEATURE:
   19 <221> NAME/KEY: CDS
   20 <222> LOCATION: (1)..(1122)
   21 <223> OTHER INFORMATION:
W--> 23 <400> 1
   24 atg gcc cgc tcg ctg acc tgg cgc tgc tgc ccc tgg tgc ctg acg gag    48
E--> 26   1           5                   10                  15
   28 gat gag aag gcc gcc gcc cgg gtg gac cag gag atc aac agg atc ctc    96
E--> 30           20                  25                  30
   32 ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg   144
E--> 34         35                  40                  45
   36 ggc cca ggc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc   192
E--> 38       50                  55                  60
   40 atc cac ggc gcc ggc tac tcg gag gag gag cgc aag ggc ttc cgg ccc   240
E--> 42   65                  70                  75                  80
   44 ctg gtc tac cag aac atc ttc gtg tcc atg cgg gcc atg atc gag gcc   288
E--> 46           85                  90                  95
   48 atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac   336
E--> 50           100                 105                 110
   52 gct agc ctg gtc atg agc cag gac ccc tat aaa gtg acc acg ttt gag   384
E--> 54           115                 120                 125
   56 aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc ggc atc   432
E--> 58           130                 135                 140
   60 cgg gcc tgc tat gag cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc   480
E--> 62   145                 150                 155                 160
   64 gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag ggc tac gtc   528
E--> 66           165                 170                 175
   68 ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act ggc atc   576
```

[handwritten right margin: amino acids. No amino acids are shown in this sequence.]

RAW SEQUENCE LISTING   DATE: 06/16/2005
PATENT APPLICATION: US/10/538,038   TIME: 10:24:46

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\06162005\J538038.raw**

```
E--> 70          180              185              190
     72 aac gag tac tgc ttc tcc gtg cag aaa acc aac ctg cgg atc gtg gac    624
E--> 74          195              200              205
     76 gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag    672
E--> 78      210              215              220
     80 aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag    720
E--> 82  225              230              235              240
     84 tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca    768
E--> 86          245              250              255
     88 ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc    816
E--> 90          260              265              270
     94 atc ctc ttt ctc aac aaa acc gac atc ctg gag gag aaa atc ccc acc    864
E--> 96      275              280              285
     98 tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat    912
E--> 100     290              295              300
    102 gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac    960
E--> 104 305              310              315              320
    106 acc ggg tgc gtg gac ggc ccc gag ggc agc aac tta aaa aaa gaa gat   1008
E--> 108     325              330              335
    110 aag gaa atc tat tct cac atg acc tgc gct act gac aca caa aac gtc   1056
E--> 112     340              345              350
    114 aaa ttc gtg ttt gat gcc gtg aca gat ata ata ata aaa gag aac ctc   1104
E--> 116     355              360              365
    118 aaa gac tgt ggg ctc ttc                                           1122
E--> 120     370
```

VERIFICATION SUMMARY   DATE: 06/16/2005
PATENT APPLICATION: **US/10/538,038**   TIME: 10:24:47

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\06162005\J538038.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21
L:26 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=1